#3 NH 5-5-00

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/480,977*

DATE: 03/17/2000
TIME: 02:47:09

INPUT SET: S35068.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao

(ii) TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and Uses Therefor

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/480,977
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/899,437
(B) FILING DATE: 24-Jul-1997

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Conley, Deirdre L.
(B) REGISTRATION NUMBER: 36,487
(C) REFERENCE/DOCKET NUMBER: P1084R1

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650/225-2066
(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2538 base pairs

(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ix) FEATURE:
(A) NAME/KEY: mouse NRG3 nucleic acid
(B) LOCATION: 1-2538
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTGACCGGC CGGCGGCGCC CGGGCCGGTC TCGCCCCTCT ACCGAGCGCC 50

TCGCCGCCCC CTCCCCGGCC CGCGTCCCCT CCCCCGTCCT CTCCTCCCCG 100

CCCGCCGCCC GCCTCTCGGG GGGAGGGGCG TGGGGGCAGG GAGCCGATTT 150

GCATGCGGCC GCCGCGGCCG CTGCCTGAGC CGGAGCCCGC CGCCGCCGGA 200

GCCCGCGCCC GCGCCCGCGC CCGGCCCGCG CGGCCCCATG CCTCTGGCGC 250

GGCCCTCGGG GGGGCGAAGG TGAAGATCGG CTCCTAGGAT GAGTGAAGGG 300

GCGGCCGGTG CCTCGCCACC TGGTGCCGCT TCGGCAGCCG CCGCCTCAGC 350

CGAGGAGGGC ACCGCGGCGG CTGCGGCGGC GGCGGCGGCG GGCGGGGGCC 400

CGGACGGCGG CGGAGAAGGG GCGGCCGAAC CCCCCCGGGA GTTACGCTGT 450

AGCGACTGCA TCGTGTGGAA CCGGCAGCAG ACGTGGTTGT GCGTGGTGCC 500

TCTGTTCATC GGCTTCATCG GCCTGGGGCT CAGCCTCATG CTGCTTAAAT 550

GGATCGTGGT AGGCTCCGTC AAGGAGTACG TGCCCACGGA CCTGGTGGAC 600

TCCAAGGGAA TGGGCCAGGA CCCCTTCTTC CTCTCCAAGC CCAGCTCTTT 650

CCCCAAGGCT ATGGAAACCA CCACAACAAC CACTTCTACC ACGTCCCCCG 700

CCACCCCCTC TGCCGGCGGC GCCGCTTCTT CCAGGACGCC TAACCGGATT 750

AGCACCCGCT TGACCACCAT CACACGGGCA CCCACCCGCT TCCCTGGGCA 800

CCGGGTTCCC ATCCGGGCTA GCCCGCGCTC TACCACAGCA CGGAACACTG 850

CTGCCCCTCC GACGGTCCTG TCCACCACGG CCCCTTTCTT CAGTAGCAGC 900

ACGCCCGGCT CCCGACCCCC GATGCCAGGA GCCCCCAGTA CGCAGGCGAT 950

GCCTTCCTGG CCCACTGCGG CGTATGCTAC CTCCTCCTAC CTCCACGATT 1000

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100  CCACTCCCTC CTGGACCCTG TCACCCTTTC AGGATGCTGC TGCCGCCTCT 1050
101
102  TCCTCCTCAC CCTCTTCCAC CTCCTCCACT ACCACCACCC CAGAAACTAG 1100
103
104  CACCAGCCCC AAATTTCATA CTACAACATA CTCCACTGAA CGATCTGAGC 1150
105
106  ACTTCAAACC CTGTCGAGAC AAGGACCTGG CGTATTGTCT CAATGATGGT 1200
107
108  GAATGCTTTG TGATTGAGAC CCTGACAGGA TCCCATAAGC ACTGTCGGTG 1250
109
110  CAAGGAAGGC TACCAAGGAG TCCGTTGTGA TCAATTTCTG CCGAAAACAG 1300
111
112  ACTCCATCTT ATCGGATCCA ACAGACCACT TGGGGATTGA ATTCATGGAG 1350
113
114  AGTGAAGACG TTTATCAAAG GCAGGTGCTG TCAATTTCAT GTATCATCTT 1400
115
116  TGGAATTGTC ATCGTGGGCA TGTTCTGTGC AGCATTCTAC TTCAAAAGCA 1450
117
118  AGAAACAAGC TAAACAAATT CAGGAGCACC TGAAAGAGTC ACAGAATGGG 1500
119
120  AAGAACTACA GCCTCAAGGC ATCCAGCACA AAGTCTGAGA GCTTGATGAA 1550
121
122  GAGCCATGTC CATCTACAAA ATTATTCAAA GGCGGATAGG CATCCTGTGA 1600
123
124  CTGCGCTGGA GAAAATAATG GAGTCAAGTT TTTCAGCTCC CCAGTCGTTC 1650
125
126  CCAGAAGTCA CTTCTCCTGA CCGAGGAAGC CAGCCTATCA AGCACCACAG 1700
127
128  CCCAGGACAA AGGAGTGGGA TGTTGCATAG GAATACTTTC AGAAGGGCAC 1750
129
130  CACCCTCACC CCGAAGTCGA CTGGGTGGTA TTGTAGGACC AGCATATCAA 1800
131
132  CAACTTGAAG AATCAAGAAT TCCAGACCAG GATACGATAC CTTGCCAAGG 1850
133
134  GATAGAGGTC AGGAAGACTA TATCCCACCT GCCTATACAG CTGTGGTGTG 1900
135
136  TTGAAAGACC CCTGGACTTA AAGTATGTGT CCAATGGCTT AAGAACCCAA 1950
137
138  CAAAATGCAT CAATAAATAT GCAACTGCCT TCAAGAGAGA CAAACCCCTA 2000
139
140  TTTTAATAGC TTGGATCAAA AGGACCTGGT GGGTTATTTA TCCCCAAGGG 2050
141
142  CCAATTCTGT GCCCATCATC CCGTCGATGG GTCTAGAAGA AACCTGCATG 2100
143
144  CAAATGCCAG GGATTTCTGA CGTCAAAAGC ATTAAATGGT GCAAAAACTC 2150
145
146  CTACTCCGCT GACATTGTCA ACGCGAGTAT GCCAGTCAGT GATTGTCTTC 2200
147
148  TAGAAGAACA ACAGGAAGTG AAAATATTAC TAGAGACTGT GCAGGAACAG 2250
149
150  ATCCGGATTC TGACTGATGC CAGACGGTCA GAAGACTTCG AACTGGCCAG 2300
151
152  CATGGAAACT GAGGACAGTG CGAGCGAAAA CACAGCCTTT CTCCCCCTGA 2350
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GTCCCACGGC CAAATCAGAA CGAGAGGCAC AATTTGTCTT AAGAAATGAA 2400

ATACAAAGAG ACTCTGTGCT AACCAAGTGA CTGGAAATGT AGGAATCTGT 2450

GCATTATATG CTTTGCTAAA CAGGAAGGAG AGGAAATTAA ATACAAATTA 2500

TTTATATGCA TTAATTTAAG AGCATCTACT TAGAAGCC 2538

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 713 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:
(A) NAME/KEY: Mouse NRG3 (mNRG3)/amino acid seq.
(B) LOCATION: 1-713
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Ser Glu Gly Ala Ala Gly Ala Ser Pro Pro Gly Ala Ala Ser
 1               5                  10                  15

Ala Ala Ala Ala Ser Ala Glu Glu Gly Thr Ala Ala Ala Ala Ala
            20                  25                  30

Ala Ala Ala Ala Gly Gly Gly Pro Asp Gly Gly Gly Glu Gly Ala
        35                  40                  45

Ala Glu Pro Pro Arg Glu Leu Arg Cys Ser Asp Cys Ile Val Trp
    50                  55                  60

Asn Arg Gln Gln Thr Trp Leu Cys Val Val Pro Leu Phe Ile Gly
65                  70                  75

Phe Ile Gly Leu Gly Leu Ser Leu Met Leu Leu Lys Trp Ile Val
            80                  85                  90

Val Gly Ser Val Lys Glu Tyr Val Pro Thr Asp Leu Val Asp Ser
        95                  100                 105

Lys Gly Met Gly Gln Asp Pro Phe Phe Leu Ser Lys Pro Ser Ser
    110                 115                 120

Phe Pro Lys Ala Met Glu Thr Thr Thr Thr Thr Thr Ser Thr Thr
125                 130                 135

Ser Pro Ala Thr Pro Ser Ala Gly Gly Ala Ala Ser Ser Arg Thr
140                 145                 150
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206
207  Pro Asn Arg Ile Ser Thr Arg Leu Thr Thr Ile Thr Arg Ala Pro
208                  155                 160                 165
209
210  Thr Arg Phe Pro Gly His Arg Val Pro Ile Arg Ala Ser Pro Arg
211                  170                 175                 180
212
213  Ser Thr Thr Ala Arg Asn Thr Ala Ala Pro Pro Thr Val Leu Ser
214                  185                 190                 195
215
216  Thr Thr Ala Pro Phe Phe Ser Ser Ser Thr Pro Gly Ser Arg Pro
217                  200                 205                 210
218
219  Pro Met Pro Gly Ala Pro Ser Thr Gln Ala Met Pro Ser Trp Pro
220                  215                 220                 225
221
222  Thr Ala Ala Tyr Ala Thr Ser Ser Tyr Leu His Asp Ser Thr Pro
223                  230                 235                 240
224
225  Ser Trp Thr Leu Ser Pro Phe Gln Asp Ala Ala Ala Ala Ser Ser
226                  245                 250                 255
227
228  Ser Ser Pro Ser Ser Thr Ser Ser Thr Thr Thr Thr Pro Glu Thr
229                  260                 265                 270
230
231  Ser Thr Ser Pro Lys Phe His Thr Thr Thr Tyr Ser Thr Glu Arg
232                  275                 280                 285
233
234  Ser Glu His Phe Lys Pro Cys Arg Asp Lys Asp Leu Ala Tyr Cys
235                  290                 295                 300
236
237  Leu Asn Asp Gly Glu Cys Phe Val Ile Glu Thr Leu Thr Gly Ser
238                  305                 310                 315
239
240  His Lys His Cys Arg Cys Lys Glu Gly Tyr Gln Gly Val Arg Cys
241                  320                 325                 330
242
243  Asp Gln Phe Leu Pro Lys Thr Asp Ser Ile Leu Ser Asp Pro Thr
244                  335                 340                 345
245
246  Asp His Leu Gly Ile Glu Phe Met Glu Ser Glu Asp Val Tyr Gln
247                  350                 355                 360
248
249  Arg Gln Val Leu Ser Ile Ser Cys Ile Ile Phe Gly Ile Val Ile
250                  365                 370                 375
25
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252    Val Gly Met Phe Cys Ala Ala Phe Tyr Phe Lys Ser Lys Lys Gln
253                    380                 385                 390
254
255    Ala Lys Gln Ile Gln Glu His Leu Lys Glu Ser Gln Asn Gly Lys
256                    395                 400                 405
257
258    Asn Tyr Ser Leu Lys Ala Ser Ser Thr Lys Ser Glu Ser Leu Met
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/480,977*

DATE: 03/17/2000
TIME: 02:47:11

INPUT SET: S35068.raw

Line	Error	Original Text

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION *US/09/480,977*

DATE: 03/17/2000
TIME: 02:47:11

INPUT SET: S35068.raw

< < THERE ARE NO ITEMS MISSING > >

SEQUENCE CORRECTION REPORT
PATENT APPLICATION *US/09/480,977*

DATE: 03/17/2000
TIME: 02:47:11

INPUT SET: S35068.raw

Line	Original Text	Corrected Text